CLAIMS

1. Method for determining the susceptibility to antiviral drugs of viruses which contain reverse transcriptase genes and are present in a biological sample, comprising:

(i) if need be releasing, isolating or concentrating the polynucleic acids present in the sample;

(ii) if need be amplifying the relevant part of the reverse transcriptase genes present in said sample with at least one suitable primer pair;

(iii) hybridizing the polynucleic acids of step (i) or (ii) with at least two RT gene probes, with said probes being applied to known locations on a solid support and with said probes being capable of simultaneously hybridizing to their respective target regions under appropiate hybridization and wash conditions allowing the detection of homologous targets, or with said probes hybridizing specifically with a sequence complementary to any of said target sequences, or a sequence wherein T of said target sequence is replaced by U;

(iv) detecting the hybrids formed in step (iii);

(v) inferring the nucleotide sequence at the codons of intrest as represented in any of Figure 1, or Tables 1, 2 or 4 and/or the amino acids of the codons of intrest and/or antiviral drug resistance spectrum, and possibly the type of viral isolates involved from the differential hybridization signal(s) obtained in step (iv).

2. Method according to claim 1, wherein said viruses are HIV strains.

3. Method according to claim 2, wherein said RT gene probes hybridize specifically to one or more target sequences as represented in any of figure 1 or tables 1, 2 or 4.

4. Method according to claim 1, wherein step (iii) consists of hybridizing with at least two probes hybridizing specifically to one or more target codons within region I as represented in Figure 1.

5. Method according to claim 1, wherein step (iii) consists of hybridizing with at least two probes hybridizing specifically to one or more target codon within region II as

represented in Figure 1.

6. Method according to claim 1, wherein step (iii) consists of hybridizing with at least two probes hybridizing specifically to one or more target codons within region III as represented in Figure 1.

7. Method according to claim 1, wherein step (iii) consists of hybridizing with at least two probes hybridizing specifically to one or more target codons within region IV as represented in Figure 1.

8. Method according to claim 1, wherein step (iii) consists of hybridizing with at least two probes hybridizing specifically to one or more target codons within region V as represented in Figure 1.

9. Method according to claim 1, wherein step (iii) consists of hybridizing with at least two probes hybridizing specifically to one or more target codons within region VI as represented in Figure 1.

10. Method according to claim 1, wherein step (iii) consists of hybridizing with at least two probes hybridizing specifically to one or more target codons within region VII as represented in Figure 1.

11. Method according to claim 1, wherein step (iii) consists of hybridizing with at least two probes hybridizing specifically to one or more target codons within region VIII as represented in Figure 1.

12. Method according to claim 1, wherein step (iii) consists of hybridizing with at least one first probe hybridizing specifically to one or more target codons within any region I to VIII as represented in Figure 1 and at least one other second probe hybridizing specifically to one or more target codons within any region I to VIII as represented in Figure 1.

13. Probe on a solid support which is suitable for hybridizing in a method as defined in

any of claims 1 to 12 and which is preferably represented in Table 3.

14. Composition comprising at least two probes according to claim 12.

15. A kit for inferring the nucleotide sequence at codons of interest in the HIV RT gene and/or the amino acids corresponding to these codons and/or the antiviral drug resistance spectrum of HIV isolates present in a biological sample comprising the following components:

(i) when appropiate, a means for releasing, isolating or concentrating the polynucleic acids present in said sample;

(ii) when appropriate, at least one of the above-defined set of primers;

(iii) at least two of the probes as defined above, possibly fixed to a solid support;

(iv) a hybridization buffer, or components necessary for producing said buffer;

(v) a wash solution, or components necessary for producing said solution;

(vi) when appropriate, a means for detecting the hybrids resulting from the preceding hybridization.

(vii) when appropriate, a means for attaching said probe to a solid support.

16. A kit for inferring the HIV RT resistance spectrum of HIV in a biological sample, coupled to the identification of the HIV isolate involved, comprising the following components:

(i) when appropiate, a means for releasing, isolating or concentrating the polynucleic acids present in the sample;

(ii) when appropriate, at least one of the sets of primers as defined above;

(iii) at least one of the probes as defined above, possibly fixed to a solid support;

(iv) a hybridization buffer, or components necessary for producing said buffer;

(v) a wash solution, or components necessary for producing said solution;

(vi) when appropriate, a means for detecting the hybrids resulting from the preceding hybridization;

(vii) when appropriate, a means for attaching said probe to a solid support.